54600-8130.US00-SEQLIST.TXT

SEQUENCE LISTING

<110> Lim, Moon Young
      Edwards, Cynthia A.
      Fry, Kirk E.
      Bruice, Thomas W.
      Starr, Douglas B.
      Laurance, Megan E.
      Kwok, Yan

<120> DNA Binding Compound-Mediated Molecular
   Switch System

<130> 4600-0130.30

<140> US 09/518,297
<141> 2000-03-03

<150> US 60/122,513
<151> 1999-03-03

<150> US 60/154,605
<151> 1999-09-17

<160> 77

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<223> n = A,T,C or G

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<210> 4
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<213> Homo sapiens

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Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln Pro Lys Gln Arg Gly Met
            20   25   30
Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser Ala Gly Ser Ile Pro Gly
        35   40   45
Glu Arg Ser Thr Asp Thr Thr Lys Thr His Pro Thr Ile Lys Ile Asn
    50   55   60
Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile Ser Leu Val Thr Lys Asp
65   70   75   80
Pro Pro His Arg Pro His Pro His Glu Leu Val Gly Lys Asp Cys Arg
                85   90   95
Asp Gly Phe Tyr Glu Ala Glu Leu Cys Pro Asp Arg Cys Ile His Ser
               100   105   110
Phe Gln Asn Leu Gly Ile Gln Cys Val Lys Lys Arg Asp Leu Glu Gln
           115   120   125
Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn Asn Pro Phe Gln Val Pro
       130   135   140
Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu Asn Ala Val Arg Leu Cys
145   150   155   160
Phe Gln Val Thr Val Arg Asp Pro Ser Gly Arg Pro Leu Arg Leu Pro
               165   170   175
Pro Val Leu Pro His Pro Ile Phe Asp Asn Arg Ala Pro Asn Thr Ala
           180   185   190
Glu Leu Lys Ile Cys Arg Val Asn Arg Asn· Ser Gly Ser Cys Leu Gly
       195   200   205
Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys Val Gln Lys Glu Asp Ile
   210   215   220
Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu Ala Arg Gly Ser Phe Ser
225   230   235   240
Gln Ala Asp Val His Arg Gln Val Ala Ile Val Phe Arg Thr Pro Pro
               245   250   255
Tyr Ala Asp Pro Ser Leu Gln Ala Pro Val Arg Val Ser Met Gln Leu
           260   265   270
Arg Arg Pro Ser Asp Arg Glu Leu Ser Glu Pro Met Glu Phe Gln Tyr
       275   280   285
Leu Pro Asp Thr Asp Asp Arg His Arg Ile Glu Glu Lys Arg Lys Arg
   290   295   300
Thr Tyr Glu Thr Phe Lys Ser Ile Met Lys Lys Ser Pro Phe Ser Gly
305   310   315   320
Pro Thr Asp Pro Arg Pro Pro Pro Arg Arg Ile Ala Val Pro Ser Arg
               325   330   335
Ser Ser Ala Ser Val Pro Lys Pro Ala Pro Gln Pro Tyr Pro Phe Thr
           340   345   350
Ser Ser Leu Ser Thr Ile Asn Tyr Asp Glu Phe Pro Thr Met Val Phe
       355   360   365
Pro Ser Gly Gln Ile Ser Gln Ala Ser Ala Leu Ala Pro Ala Pro Pro
   370   375   380

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Gln Val Leu Pro Gln Ala Pro Ala Pro Ala Pro Ala Pro Ala Met Val
385             390             395             400
Ser Ala Leu Ala Gln Ala Pro Ala Pro Val Pro Val Leu Ala Pro Gly
            405             410             415
Pro Pro Gln Ala Val Ala Pro Pro Ala Pro Lys Pro Thr Gln Ala Gly
            420             425             430
Glu Gly Thr Leu Ser Glu Ala Leu Leu Gln Leu Gln Phe Asp Asp Glu
            435             440             445
Asp Leu Gly Ala Leu Leu Gly Asn Ser Thr Asp Pro Ala Val Phe Thr
450             455             460
Asp Leu Ala Ser Val Asp Asn Ser Glu Phe Gln Gln Leu Leu Asn Gln
465             470             475             480
Gly Ile Pro Val Ala Pro His Thr Thr Glu Pro Met Leu Met Glu Tyr
            485             490             495
Pro Glu Ala Ile Thr Arg Leu Val Thr Gly Ala Gln Arg Pro Pro Asp
            500             505             510
Pro Ala Pro Ala Pro Leu Gly Ala Pro Gly Leu Pro Asn Gly Leu Leu
            515             520             525
Ser Gly Asp Glu Asp Phe Ser Ser Ile Ala Asp Met Asp Phe Ser Ala
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Leu Leu Ser Gln Ile Ser Ser
545             550
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<212> DNA
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<220>
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cttaacactc gcgagtgtta ag                                          22

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<221> misc_feature
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<223> n = A or C

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<211> 77
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Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp Gly
 1   5   10   15
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            20   25   30
Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro His
        35   40   45
Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe Glu
    50   55   60
Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Glu Tyr Gly
65   70   75

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Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu
 1   5   10

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<212> PRT
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<220>
<223> repressor sequence

<400> 10
Met Asp Ala Lys Ser Leu Thr Ala Trp Ser Arg Thr Leu Val Thr Phe
 1   5   10   15
Lys Asp Val Phe Val Asp Phe Thr Arg Glu Glu Trp Lys Leu Leu Asp
            20   25   30
Thr Ala Gln Gln Ile Val Tyr Arg Asn Val Met Leu Glu Asn Tyr Lys
        35   40   45
Asn Leu Val Ser Leu Gly Tyr Gln Leu Thr Lys Pro Asp Val Ile Leu
    50   55   60
Arg Leu Glu Lys Gly Glu Glu Pro Trp Leu Val Glu Arg Glu Ile His
65   70   75   80
Gln Glu Thr His Pro Asp Ser Glu Thr Ala Phe Glu Ile Lys Ser Ser
                85   90   95
Val

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<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> repressor sequence

<400> 11
Met Ala Ala Ala Val Arg Met Asn Ile Gln Met Leu Leu Glu Ala Ala
1               5                   10                  15
Asp Tyr Leu Glu Arg Arg Glu Arg Glu Ala Glu His Gly Tyr Ala Ser
            20                  25                  30
Met Leu Pro Tyr
        35

<210> 12
<211> 116
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (0)...(0)
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<400> 12
cgcggtcaga aaattatttt aaatttcctc ttgtcaggcc ggaataactc cctataatgc    60
gccaccactg acacggaaca acggcaaaca cgccgccggg tcagcggggt tctcct       116

<210> 13
<211> 22
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (0)...(0)
<223> partial promoter sequence

<400> 13
agaaaattat tttaaatttc ct                                            22

<210> 14
<211> 22
<212> DNA
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<220>
<223> modified promoter sequence

<400> 14
gactgcagtg gtacctagga gg                                            22

<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> modified promoter sequence
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<400> 15
agaaaattat tttaaatttc ct   22

<210> 16
<211> 22
<212> DNA
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<220>
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<400> 16
ggaaaatttt ttttcaaaag ta   22

<210> 17
<211> 22
<212> DNA
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<220>
<223> modified promoter sequence

<400> 17
tgaaatttat tttgcgaaag gg   22

<210> 18
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<213> Artificial Sequence

<220>
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<400> 18
tgttcgcact t   11

<210> 19
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 19
catggacgcc actgagccgt ttttgttcgc acttgaggcg agtcgatgca cc   52

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<212> DNA
<213> Artificial Sequence

<220>
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<400> 20
catggacgcc actgagccgt gttcgcactt tttttttgagg cgagtcgatg cacc   54

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<212> DNA
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<400> 22
cttaaaaata ac   12

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<212> DNA
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<400> 23
ttgaaaaatc aacgct   16

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<400> 24
tttttgttcg cacttttttt t   21

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<400> 25
tttttgggat tttcctttttt   20

<210> 26
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 26
aaaaaattgt gagcgctcac aatttttt   28

<210> 27

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<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> tissue-specific transcription factor

<400> 27
acttta                                                                    6

<210> 28
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<213> Artificial Sequence

<220>
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<400> 28
taccgacat                                                                 9

<210> 29
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

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gggactttcc                                                               10

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<220>
<223> engineered DNA response element

<400> 30
gggattttcc                                                               10

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<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 31
cgaccgtgct cgagttaacg ggactttcca aaaacgatcg gactggactc                  50

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<400> 32
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cgaccgtgct cgagttaacg ggattttcca aaaacgatcg gactggactc   50

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cgaccgtgct cgagaaattg ggattttcca aaaacgatcg gactggactc   50

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<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 34
aaaaaattgt gagcgctcac aatttttt   28

<210> 35
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 35
ttttttttgt gagcggataa caaaa   25

<210> 36
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<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 36
tctgggatcc   10

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<212> DNA
<213> Artificial Sequence

<220>
<223> engineered DNA response element

<400> 37
gagttttttt taag   14

<210> 38
<211> 14
<212> DNA
<213> Artificial Sequence

<220>

<223> engineered DNA response element

<400> 38
gagttttaaa agag   14

<210> 39
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<213> Homo sapiens

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<223> transcriptional regulatory protein

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 1   5   10   15
Leu Asp Pro Ser Leu Thr His Thr Ile Phe Asn Pro Glu Val Phe Gln
            20   25   30
Pro Gln Met Ala Leu Pro Thr Ala Asp Gly Pro Tyr Leu Gln Ile Leu
            35   40   45
Glu Gln Pro Lys Gln Arg Gly Phe Arg Phe Arg Tyr Val Cys Glu Gly
        50   55   60
Pro Ser His Gly Gly Leu Pro Gly Ala Ser Ser Glu Lys Asn Lys Lys
65   70   75   80
Ser Tyr Pro Gln Val Lys Ile Cys Asn Tyr Val Gly Pro Ala Lys Val
                85   90   95
Ile Val Gln Leu Val Thr Asn Gly Lys Asn Ile His Leu His Ala His
            100   105   110
Ser Leu Val Gly Lys His Cys Glu Asp Gly Ile Cys Thr Val Thr Ala
            115   120   125
Gly Pro Lys Asp Met Val Val Gly Phe Ala Asn Leu Gly Ile Leu His
        130   135   140
Val Thr Lys Lys Lys Val Phe Glu Thr Leu Glu Ala Arg Met Thr Glu
145   150   155   160
Ala Cys Ile Arg Gly Tyr Asn Pro Gly Leu Leu Val His Pro Asp Leu
                165   170   175
Ala Tyr Leu Gln Ala Glu Gly Gly Gly Asp Arg Gln Leu Gly Asp Arg
            180   185   190
Glu Lys Glu Leu Ile Arg Gln Ala Ala Leu Gln Gln Thr Lys Glu Met
            195   200   205
Asp Leu Ser Val Val Arg Leu Met Phe Thr Ala Phe Leu Pro Asp Ser
        210   215   220
Thr Gly Ser Phe Thr Arg Arg Leu Glu Pro Val Val Ser Asp Ala Ile
225   230   235   240
Tyr Asp Ser Lys Ala Pro Asn Ala Ser Asn Leu Lys Ile Val Arg Met
                245   250   255
Asp Arg Thr Ala Gly Cys Val Thr Gly Gly Glu Glu Ile Tyr Leu Leu
            260   265   270
Cys Asp Lys Val Gln Lys Asp Asp Ile Gln Ile Arg Phe Tyr Glu Glu
        275   280   285
Glu Glu Asn Gly Gly Val Trp Glu Gly Phe Gly Asp Phe Ser Pro Thr
        290   295   300
Asp Val His Arg Gln Phe Ala Ile Val Phe Lys Thr Pro Lys Tyr Lys
305   310   315   320
Asp Ile Asn Ile Thr Lys Pro Ala Ser Val Phe Val Gln Leu Arg Arg
                325   330   335
Lys Ser Asp Leu Glu Thr Ser Glu Pro Lys Pro Phe Leu Tyr Tyr Pro
            340   345   350
Glu Ile Lys Asp Lys Glu Glu Val Gln Arg Lys Arg Gln Lys Leu Met
            355   360   365
Pro Asn Phe Ser Asp Ser Phe Gly Gly Gly Ser Gly Ala Gly Ala Gly
                          Page 10

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          370                      375                      380
Gly Gly Gly Met Phe Gly Ser Gly Gly Gly Gly Gly Thr Gly Ser
385                      390                      395                      400
Thr Gly Pro Gly Tyr Ser Phe Pro His Tyr Gly Phe Pro Thr Tyr Gly
                        405                      410                      415
Gly Ile Thr Phe His Pro Gly Thr Thr Lys Ser Asn Ala Gly Met Lys
                420                      425                      430
His Gly Thr Met Asp Thr Glu Ser Lys Lys Asp Pro Glu Gly Cys Asp
            435                      440                      445
Lys Ser Asp Asp Lys Asn Thr Val Asn Leu Phe Gly Lys Val Ile Glu
450                      455                      460
Thr Thr Glu Gln Asp Gln Glu Pro Ser Glu Ala Thr Val Gly Asn Gly
465                      470                      475                      480
Glu Val Thr Leu Thr Tyr Ala Thr Gly Thr Lys Glu Glu Ser Ala Gly
                485                      490                      495
Val Gln Asp Asn Leu Phe Leu Glu Lys Ala Met Gln Leu Ala Lys Arg
                500                      505                      510
His Ala Asn Ala Leu Phe Asp Tyr Ala Val Thr Gly Asp Val Lys Met
            515                      520                      525
Leu Leu Ala Val Gln Arg His Leu Thr Ala Val Gln Asp Glu Asn Gly
            530                      535                      540
Asp Ser Val Leu His Leu Ala Ile Ile His Leu His Ser Gln Leu Val
545                      550                      555                      560
Arg Asp Leu Leu Glu Val Thr Ser Gly Leu Ile Ser Asp Asp Ile Ile
                565                      570                      575
Asn Met Arg Asn Asp Leu Tyr Gln Thr Pro Leu His Leu Ala Val Ile
                580                      585                      590
Thr Lys Gln Glu Asp Val Val Glu Asp Leu Leu Arg Ala Gly Ala Asp
            595                      600                      605
Leu Ser Leu Leu Asp Arg Leu Gly Asn Ser Val Leu His Leu Ala Ala
            610                      615                      620
Lys Glu Gly His Asp Lys Val Leu Ser Ile Leu Leu Lys His Lys Lys
625                      630                      635                      640
Ala Ala Leu Leu Leu Asp His Pro Asn Gly Asp Gly Leu Asn Ala Ile
                645                      650                      655
His Leu Ala Met Met Ser Asn Ser Leu Pro Cys Leu Leu Leu Leu Val
            660                      665                      670
Ala Ala Gly Ala Asp Val Asn Ala Gln Glu Gln Lys Ser Gly Arg Thr
            675                      680                      685
Ala Leu His Leu Ala Val Glu His Asp Asn Ile Ser Leu Ala Gly Cys
            690                      695                      700
Leu Leu Leu Glu Gly Asp Ala His Val Asp Ser Thr Thr Tyr Asp Gly
705                      710                      715                      720
Thr Thr Pro Leu His Ile Ala Ala Gly Arg Gly Ser Thr Arg Leu Ala
                725                      730                      735
Ala Leu Leu Lys Ala Ala Gly Ala Asp Pro Leu Val Glu Asn Phe Glu
                740                      745                      750
Pro Leu Tyr Asp Leu Asp Asp Ser Trp Glu Asn Ala Gly Glu Asp Glu
            755                      760                      765
Gly Val Val Pro Gly Thr Thr Pro Leu Asp Met Ala Thr Ser Trp Gln
            770                      775                      780
Val Phe Asp Ile Leu Asn Gly Lys Pro Tyr Glu Pro Glu Phe Thr Ser
785                      790                      795                      800
Asp Asp Leu Leu Ala Gln Gly Asp Met Lys Gln Leu Ala Glu Asp Val
                805                      810                      815
Lys Leu Gln Leu Tyr Lys Leu Leu Glu Ile Pro Asp Pro Asp Lys Asn
                820                      825                      830
Trp Ala Thr Leu Ala Gln Lys Leu Gly Leu Gly Ile Leu Asn Asn Ala
            835                      840                      845
Phe Arg Leu Ser Pro Ala Pro Ser Lys Thr Leu Met Asp Asn Tyr Glu
850                      855                      860
Val Ser Gly Gly Thr Val Arg Glu Leu Val Glu Ala Leu Arg Gln Met
865                      870                      875                      880
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Gly Tyr Thr Glu Ala Ile Glu Val Ile Gln Ala Ala Ser Ser Pro Val
              885                 890                 895
Lys Thr Thr Ser Gln Ala His Ser Leu Pro Leu Ser Pro Ala Ser Thr
          900                 905                 910
Arg Gln Gln Ile Asp Glu Leu Arg Asp Ser Asp Ser Val Cys Asp Thr
          915                 920                 925
Gly Val Glu Thr Ser Phe Arg Lys Leu Ser Phe Thr Glu Ser Leu Thr
      930                 935                 940
Ser Gly Ala Ser Leu Leu Thr Leu Asn Lys Met Pro His Asp Tyr Gly
945                 950                 955                 960
Gln Glu Gly Pro Leu Glu Gly Lys Ile
                  965
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<211> 96
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<220>
<223> engineered regulatory sequence

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agcagagctc gtttagtgaa ccgtcagatc agatct                              96
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<212> DNA
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<220>
<223> engineered regulatory sequence

<400> 41
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atcgcccgcc ccgttgacgc aaatgggcgg taggcgtgta cggtgggagg tttatataag   120
cagagctcgt ttagtgaacc gtcagatcag atct                               154
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<210> 42
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<213> Artificial Sequence

<220>
<223> engineered regulatory sequence

<400> 42
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tagcgcccaa attgggattt tccaaaaagc cgaaattggg attttccaaa aaccgccgat   120
cgcccgcccc gttgacgcaa atgggcggta ggcgtgtacg gtgggaggtt tatataagca   180
gagctcgttt agtgaaccgt cagatcagat ct                                 212
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<210> 43
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 43
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agcagagctc gtttagtgaa ccgtcagatc agatct                              96
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atcgcccgcc ccgttgacgc aaatgggcgg taggcgtgta cggtgggagg cctatataag     120
cagagctcgt ttagtgaacc gtcagatcag atct                                 154

<210> 45
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<212> DNA
<213> Artificial Sequence

<220>
<223> engineered regulatory sequence

<400> 45
gctagcgccc aggtcgggat tttccgagga gccgaggtcg ggattttccg aggaccgccg      60
atcgcccgcc ccgttgacgc aaatgggcgg taggcgtgta cggtgggagg cctatataag     120
cagagctcgt ttagtgaacc gtcagatcag atct                                 154

<210> 46
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<212> DNA
<213> Artificial Sequence

<220>
<223> engineered promoter construct

<400> 46
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tggctattgg ccattgcata cgttgtatct atatcataat atgtacattt atattggctc     120
atgtccaata tgaccgccat gttggcattg attattgact agttattaat agtaatcaat     180
tacggggtca ttagttcata gcccatatat ggagttccgc gttacataac ttacggtaaa     240
tggcccgcct ggctgaccgc ccaacgaccc ccgcccattg acgtcaataa tgacgtatgt     300
tcccatagta acgcaaatag ggattttcca ttaacgtcaa tgggtggagt atttacggta     360
aactgcccac ttggcagtac atcaagtgta tcatatgcca gtccgcccc ctattgacgt      420
caatgacggt aaatggcccg cctggcatta tgcccagtac atgactttat gggattttcc     480
tatttggcag tacatctacg tattagtcat cgctattacc atggtgatgc ggttttggca     540
gtacaccaat gggcgtggat agcggtttga ctcacgggga tttccaagtc tccaccccat     600
tgacgtcaat gggagtttgt tttggcacca aggtaaaagg gattttccaa aatgtcgtaa     660
caactgcgat cgcccgcccc gttgacgcaa atgggcggta ggcgtgtacg gtgggaggtt     720
tatataagca gagctcgttt agtgaaccgt cagatcaagc tt                        762

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<400> 47
ggtacctcaa tattggccat tagccatatt attcattggt tatatagcat aaattaatat      60
tggctattgg ccattgcata cgttgtatct atatcataat atgtacattt atattggctc     120
atgtccaata tgaccgccat gttggcattg attattgact agttattaat agtaatcaat     180
tacggggtca ttagttcata gcccatatat ggagttccgc gttacataac ttacggtaaa     240
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tggcccgcct ggctgaccgc ccaacgaccc ccgcccattg acgtcaataa tgacgtatgt    300
tcccatagta acgcaaatat tcccgggaaa ttaacgtcaa tgggtggagt atttacggta    360
aactgcccac ttggcagtac atcaagtgta tcatatgcca agtccgcccc ctattgacgt    420
caatgacggt aaatggcccg cctggcatta tgcccagtac atgactttat tctcgaggaa    480
tatttggcag tacatctacg tattagtcat cgctattacc atggtgatgc ggttttggca    540
gtacaccaat gggcgtggat agcggtttga ctcacgggga tttccaagtc tccaccccat    600
tgacgtcaat gggagtttgt tttggcacca aggtaaaatt acgcgtaaaa aatgtcgtaa    660
caactgcgat cgcccgcccc gttgacgcaa atgggcggta ggcgtgtacg gtgggaggtt    720
gctagccgca gagctcgttt agtgaaccgt cagatcaagc tt                       762
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<213> Artificial Sequence

<220>
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                20                  25                  30
Leu Glu Met Leu Gly Asp Val Glu Ser Pro Ser Pro Gly Met Thr His
            35                  40                  45
Asp Pro Val Ser Tyr Gly Ala Leu Asp Val Asp Asp Phe Glu Phe Glu
        50                  55                  60
Gln Met Phe Thr Asp Ala Leu Gly Ile Asp Asp Phe Gly
65                  70                  75

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<212>  PRT
<213>  Herpes simplex virus type 2

<400>  64
Ala Asp Ala Leu Asp Asp Phe Asp Leu Glu Met Ala Asp Ala Leu Asp
1               5                   10                  15
Asp Phe Asp Leu Glu Met Ala Asp Ala Leu Asp Asp Phe Asp Leu Glu
                20                  25                  30
Met Ala Asp Ala Leu Asp Asp Phe Asp Leu Glu Met
            35                  40

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<400> 76
gagtttt   7

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<220>
<223>  sequence complementary to SEQ ID No:33

<400>  77
aaaacttta                                                              9
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